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STIC-Biotech/ChemLib

From: ~~Gibbs, Terra~~
Sent: Friday, November 08, 2002 1:18 PM
T: STIC-Biotech/ChemLib
Subject: Sequence search....

1. Could you please do an oligomer search of Serial number 09/918026 (SEQ ID NO: 3)

2. Please do a length limited search of 100 nucleobases or less.

HAND or ALSO
Terra Gibbs #79523
AU 1635 ✓
Mailbox 11E12 ✓
306-3221

out unit
please

THANK YOU!

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Dear Ms. Gibbs

I assumed perhaps incorrectly that you
wanted one search run of an oligomer with a size limit of 100 or less.

If you wanted 2 searches

1. an oligomer
2. a length limited search

please let me know & I'll redo this for you. In future if you
could number the various pieces of your request as shown above
this would be a clearer indicator of the different pieces of your request.
This is what most other seminars do to differentiate the various queries.

Thanks.

Toby Port
308-3534

Alternatively, start the next request with the word ALSO or AMD.

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 11/12
Date Completed: 11/15
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 14, 2002, 18:57:56 ; Search time 2874 Seconds
(without alignments)
15888.066 Million cell updates/sec
Title: US-09-918-026A-3
Perfect score: 1569
Sequence: 1 atgagccagcggggccg.....cttggctcgtccatacctag 1569
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 2054640 seqs, 14551402878 residues
Word size : 0
Total number of hits satisfying chosen parameters: 995600
Minimum DB seq length: 0
Maximum DB seq length: 100
Post-processing: Listing first 45 summaries

Database :

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2	58	3.7	96	9	F331502S02
3	55	3.5	100	9	F331502S07
4	54	3.4	90	9	F331502S15
5	49	3.1	91	9	F331502S09
6	18	1.1	83	9	HSA27254
7	15	1.0	18	6	E25757
8	15	1.0	20	6	AX418779
9	15	1.0	24	6	AX428505
10	15	1.0	25	6	AX223975
11	15	1.0	30	6	E30087
12	15	1.0	31	6	AX247925
13	15	1.0	31	6	AX398736
14	15	1.0	32	6	A84491
15	15	1.0	32	6	AX427390
16	15	1.0	40	6	A48829
17	15	1.0	51	6	AX157211
18	15	1.0	51	6	AX157212
19	15	1.0	51	6	AX164830
20	15	1.0	51	6	AX199127
21	15	1.0	51	6	AX199128
22	15	1.0	51	6	AX392886
23	15	1.0	56	6	AX473971
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26	15	1.0	80	6	AR030463
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35	14	0.9	18	6	I69013
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37	14	0.9	19	6	AX363014
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43	14	0.9	23	6	BD008422
44	14	0.9	24	6	AR092060
45	14	0.9	24	6	AR112195

ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene,
exon 4,
AF331505.1 GI:13310366
ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 100)
Katsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T.,

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Niikawa,N. and Ohta,T.
Structure of the human acyl-CoA:cholesterol acyltransferase-2
(ACAT-2) gene and its relation to dyslipidemia
Unpublished
2 (bases 1 to 100)
Katsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T.,
Niikawa,N. and Ohta,T.
Direct Submission
Submitted (22-DEC-2000) Department of Pediatrics, Faculty of
Medicine, University of the Ryukyus, 207 Uehara, Nishihara, Okinawa
903-0125, Japan
Location/Qualifiers
1. .100
/organism="Homo sapiens"
/db_xref="taxon:9606"
21. .80
/gene="SOAT2"
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 18 CAGGACCCAGAGCCATCCCTGGGGAACAGAAAGTTTCATCATCCGAGTCCCTGCT 77
Qy 333 TGA 335
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Db 78 TGA 80
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F331502S02
LOCUS F331502S02 96 bp DNA linear PRI 13-MAR-2001
DEFINITION Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene,
exon 2.
ACCESSION AF331503
VERSION AF331503.1 GI:13310364
KEYWORDS
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Homo sapiens.
Homo sapiens.
REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Katsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T.,
Niikawa,N. and Ohta,T.
Direct Submission
Submitted (22-DEC-2000) Department of Pediatrics, Faculty of
Medicine, University of the Ryukyus, 207 Uehara, Nishihara, Okinawa
903-0125, Japan
Location/Qualifiers
1. .96
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26 a 27 c 27 g 16 t
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Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS F331502S07 100 bp DNA linear PRI 13-MAR-2001
DEFINITION Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene,
exon 7.
ACCESSION AF331508
VERSION AF331508.1 GI:13310369
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens.
Homo sapiens.
Homo sapiens.
REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Katsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T.,
Niikawa,N. and Ohta,T.
Direct Submission
Submitted (22-DEC-2000) Department of Pediatrics, Faculty of
Medicine, University of the Ryukyus, 207 Uehara, Nishihara, Okinawa
903-0125, Japan
Location/Qualifiers
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RESULT 4
F331502S15
LOCUS F331502S15 90 bp DNA linear PRI 13-MAR-2001
DEFINITION Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene,
exon 15 and complete cds.
ACCESSION AF331516
VERSION AF331516.1 GI:13310377
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens.
Homo sapiens.
Homo sapiens.
REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Katsuren,K., Tamura,T., Arashiro,R., Takata,K., Matsuura,T.,
Niikawa,N. and Ohta,T.
Direct Submission
Submitted (22-DEC-2000) Department of Pediatrics, Faculty of
Medicine, University of the Ryukyus, 207 Uehara, Nishihara, Okinawa
903-0125, Japan
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.1e-21;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TITLE	Direct Submission									
JOURNAL	Submitted (22-DEC-2000) Department of Pediatrics, Faculty of Medicine, University of the Ryukyus, 207 Uehara, Nishihara, Okinawa 903-0125, Japan									
FEATURES	Location/Qualifiers									
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RESULT 5										
F331502S09										
LOCUS	F331502S09 91 bp DNA linear PRI 13-MAR-2001									
DEFINITION	Homo sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2) gene, exon 9.									
ACCESSION	AF331510									
VERSION	AF331510.1 GI:13310371									
KEYWORDS										
SEGMENT										
9 of 15										
Homo sapiens.										

Fri Nov 15 09:17:43 2002

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QY 649 CACGTGGCGTGGAGCAT 666
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Db 27 CACGTGGCGTGGAGCAT 10

RESULT 7
E25757/c
LOCUS E25757 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for the type classification of hepatitis B viruses and
            primer and probe to be used therein.
ACCESSION E25757
VERSION E25757.1 GI:13024945
KEYWORDS JP 1999103898-A/14.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Masakazu, M., Kazumasa, H., Kenichi, O. and Masashi, M.
TITLE Method for the type classification of hepatitis B viruses and
JOURNAL primer and probe to be used therein
COMMENT Patent: JP 1999103898-A 14 20-APR-1999;
SRL INC
OS Unidentified
PN JP 1999103898-A/14
PD 20-APR-1999
PF 30-SEP-1997 JP 1997282784
PR MASAKAZU MUKAIDE, KAZUMASA HIKIJI, KENICHI OBA, MASASHI MIZOUE PC
PI C12Q1/70, C12N15/09, G01N33/576, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 AGGTTCTTGAGCAG 275
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RESULT 8
AX418779/c
LOCUS AX418779 20 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 174 from Patent WO0210378.
ACCESSION AX418779
VERSION AX418779.1 GI:21523642
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS Cowser, L.M., Wyatt, J., Freier, S.M., Monia, B.P., Butler, M.M. and
McKay, R.
TITLE Antisense modulation of ptp1b expression
JOURNAL Patent: WO 0210378-A 174 07-FEB-2002;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES
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/organism='synthetic construct'
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DEFINITION Sequence 71 from Patent WO0233084.
ACCESSION AX428505
VERSION AX428505.1 GI:21538454
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS Reid, M.E., Gubin, A. and Miller, J.L.
TITLE Identification of the dombrock blood group glycoprotein as a
JOURNAL polymorphic member of the adp-ribosyltransferase gene family
COMMENT Patent: WO 0233084-A 71 25-APR-2002; THE UNITED STATES (US)
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LOCUS AX223975 25 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 16 from Patent WO0157221.
ACCESSION AX223975
VERSION AX223975.1 GI:15551642
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
            artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Luche, R.M. and Wei, B.
TITLE Dsp-12 and dsp-13 dual-specificity phosphatases
JOURNAL Patent: WO 0157221-A 16 09-AUG-2001;
Ceptyr, Inc. (US)
FEATURES
source
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BASE COUNT 4 a 3 c 15 g 3 t
ORIGIN

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QY 244 CTGCCCCCACCTCCC 258
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Db 22 CTGCCCCCACCTCCC 8

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E30087
LOCUS       Human BMP-7 promoter and method for detecting bone-associated
DEFINITION substance by using the same Human BMP-7 promoter and method for
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ACCESSION   E30087
VERSION     1
KEYWORDS    unclassified.
SOURCE      unclassified.
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Shinji,K. and Takeyuki,S.
TITLE       Human BMP-7 promoter and method for detecting bone-associated
JOURNAL     Patent: JP 199313675-A 2 16-NOV-1999;
COMMENT     HOECHST MARION ROUSSEL GMBH
OS          Unidentified
PN          JP 199313675-A/2
PD          16-NOV-1999
PF          30-APR-1998 JP 1998120174
PR
PI          SHINJI KAWAI, TAKEYUKI SUGIURA
PC          C12N15/09, C12N5/10, C12Q1/68//A61K48/00, (C12N5/10, C12R1:91), PC
              C12N15/00,
PC          C12N5/00, (C12N5/00, C12R1:91)
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CC          Topology: Linear;
FH          Key
FT          source
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QY 11 GCGGGGCCGCTGTC 25
Db 8 GCGGGGCCGCTGTC 22

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LOCUS       AX247925
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ACCESSION   AX247925
VERSION     1
KEYWORDS    unclassified.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 31)
AUTHORS     Cargili,M., Ireland,J.S. and Lander,E.S.
TITLE       Human single nucleotide polymorphisms
JOURNAL     Patent: WO 0166800-A 4 13-SEP-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES    Location/Qualifiers
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Db 8 GCGGGGCCGCTGTC 22

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DEFINITION Sequence 28 from Patent WO0220786.
ACCESSION   AX398736
VERSION     1
KEYWORDS    synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Schiavo,G.M. and Iglesias,T.I.
TITLE       Kinase d interacting protein
JOURNAL     Patent: WO 0220786-A 28 14-MAR-2002;
            IMPERIAL CANCER RESEARCH TECHNOLOGY LIMITED (GB)
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QY 732 CTCCTTCCTGAGAGA 746
Db 17 CTCCTTCCTGAGAGA 31

RESULT 14
A84491/c
LOCUS       A84491
DEFINITION Sequence 106 from Patent WO9845704.
ACCESSION   A84491
VERSION     1
KEYWORDS    unclassified.
SOURCE      unclassified.
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 32)
AUTHORS     Tullin,S. and Kasper,A.
TITLE       A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN
            INFLUENCE ON A CELLULAR RESPONSE
JOURNAL     Patent: WO 9845704-A 106 15-OCT-1998;
            TULLIN SOEREN (DK); KASPER ALMHOLT (DK)
FEATURES    Location/Qualifiers
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QY 749 CTGTGCTGGGATCC 763
Db 17 CTGTGCTGGGATCC 3
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RESULT 15
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LOCUS Sequence 106 from Patent EP1199564.
DEFINITION AX427390
ACCESSION AX427390
VERSION AX427390.1 GI:21530743
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
unclassified.
REFERENCE 1
AUTHORS Thastum,O., Bjoern,S.P., Tullin,S., Almholt,K. and Scudder,K.
TITLE A method for screening substances for effect on intracellular
translocation
JOURNAL Patent: EP 1199564-A 106 24-APR-2002;
Biolmage A/S (DK)
FEATURES
source
1..32
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 749 CTGTGCGCTGGGATCC 763
|||||
Db 17 CTGTGCGCTGGGATCC 3

Search completed: November 14, 2002, 20:23:03
Job time : 2877 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 18:10:46 ; Search time 254 Seconds
(without alignments)
13910.966 Million cell updates/sec

Title: US-09-918-026A-3

Perfect score: 1569

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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- 22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	3.8	60	ABN36849	Human spliced tran
2	24	1.5	25	AAA76178	Human ACAT Related
3	23	1.5	23	AAA76183	Human ACAT Related
4	20	1.3	20	AAZ57363	Human acyl CoA:cho
5	20	1.3	20	AAZ57364	Human acyl CoA:cho
6	17	1.1	65	ABN28762	Rat spliced transc
7	16	1.0	20	AAZ77373	Human biallelic ma
8	16	1.0	60	AAV21372	Immunoglobulin genom
9	16	1.0	87	ABA50541	Human breast cell

10	16	1.0	87	22	ABAG68500	Human foetal liver
11	16	1.0	87	22	ABAK35481	Probe #13947 for g
12	16	1.0	87	22	ABAK16867	Human brain expres
13	16	1.0	87	22	AAK42636	Human bone marrow
14	16	1.0	87	22	AAI23392	Probe #13325 for g
15	16	1.0	87	22	AAI48715	Probe #17401 used
16	16	1.0	87	22	AAI09020	Probe #9011 used t
17	16	1.0	87	24	ABSI6691	Human genome-deriv
18	15	1.0	17	19	AAV97364	Human EGF-R target
19	15	1.0	18	20	AAZ37843	PCR primer #2 from
20	15	1.0	18	20	AAZ55895	Hepatitis B virus
21	15	1.0	20	22	AAI21117	Rat PTPIB antisens
22	15	1.0	20	24	ABK85192	Rat PTPIB antisens
23	15	1.0	20	24	AAZ36657	Human Her-1 antis
24	15	1.0	20	24	ABK37361	Rat PTPIB mRNA lev
25	15	1.0	22	24	AAZ38835	Human PSNA cDNA, p
26	15	1.0	23	20	AAZ76655	Human spv library
27	15	1.0	24	24	ABN88782	Porphobilinogen de
28	15	1.0	25	22	AAI22975	Human DSP-12 cDNA
29	15	1.0	25	24	ABQ61310	Human aquaporin 5
30	15	1.0	27	19	AAV25385	Primer B13 of the
31	15	1.0	30	21	AAZ55621	Human BMP-7 exon 1
32	15	1.0	31	22	AAI29516	Human single nucle
33	15	1.0	31	24	ABK51212	Rat kidns220 C-te
34	15	1.0	32	19	AAV71069	Primer zap70-botto
35	15	1.0	33	24	ABK47693	Human RING finger
36	15	1.0	40	17	AAI13190	Human insulin codi
37	15	1.0	40	22	AAI17998	A. fumigatus codon
38	15	1.0	41	20	AAZ76664	Human spv library
39	15	1.0	41	24	ABK47695	Human RING finger
40	15	1.0	46	21	AAZ94217	PAPF1-TfeAFP gene
41	15	1.0	48	19	AAV30382	Oligomer p48rg20 u
42	15	1.0	48	21	AAZ87105	Rat hepatocyte car
43	15	1.0	51	22	AAI73598	Human silent SNP c
44	15	1.0	51	22	AAI73599	Human silent SNP c
45	15	1.0	51	22	AAH89276	Human coding sequ

ALIGNMENTS

RESULT 1
ABN36849
ID ABN36849 standard; DNA; 60 BP.
XX
AC ABN36849;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:9597.
XX
KW Human; mouse; rat; splice transcript; detection: RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
PN WO200210449-A2.
PD 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of

PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 9597; 47pp; English.
XX

CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

XX Sequence 60 BP; 7 A; 21 C; 10 G; 22 T; 0 other;

Query Match 3.8%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 TATCCTGCATGCCAGGTGCCAGGCATCTTCATGCTGCTCATCTCTTGGCTTCCT 1076
|||||
Db 1 TATCCTGCATGCCAGGTGCCAGGCATCTTCATGCTGCTCATCTCTTGGCTTCCT 60

RESULT 2
AAA76178
ID AAA76178 standard; DNA; 25 BP.
XX
AC AAA76178;
XX
DT 14-DEC-2000 (first entry)
XX
DE Human ACAT Related Gene Product 2 ARG2 PCR primer 206.
XX
KW Human; ACAT Related Gene Product 2; ARG2;
KW enzyme; acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
KW sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
KW DGAT; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6100077-A.
XX
PD 08-AUG-2000.
XX
PF 01-OCT-1998; 98US-0165042.
XX
PR 01-OCT-1998; 98US-0165042.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Sturley SL, Oelkers P;
XX
DR WPI; 2000-557622/51.
XX
PT New nucleic acid encoding a human diacylglycerol acyltransferase,

PT useful for treating hyperlipidemia, atherosclerosis, heart disease, or
PT other diseases associated with an imbalance of triglyceride levels -
XX
PS Disclosure; Column 17; 32pp; English.
XX
CC The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1)
CC mediates sterol esterification, an important component of intracellular
CC lipid homeostasis. The present invention relates to human ACAT Related
CC Gene Product 2 (ARGP2). ARGP2 is a diacylglycerol acyltransferase
CC (DGAT). ARGP2 is a tissue specific sterol esterification enzyme. The
CC present sequence is a PCR primer used to isolate ARGP2 coding sequence
CC (see AAA76170).

XX Sequence 25 BP; 3 A; 8 C; 4 G; 10 T; 0 other;

Query Match 1.5%; Score 24; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1047 CATGCTGCTCATCTCTTTCG 1070
|||||
Db 1 CATGCTGCTCATCTCTTTCG 24

RESULT 3
AAA76183
ID AAA76183 standard; DNA; 23 BP.
XX
AC AAA76183;
XX

XX 14-DEC-2000 (first entry)

XX Human ACAT Related Gene Product 2 ARG2 PCR primer 201.

XX Human; ACAT Related Gene Product 2; ARG2;

XX enzyme; acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
XX sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
XX DGAT; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6100077-A.
XX
PD 08-AUG-2000.
XX
PF 01-OCT-1998; 98US-0165042.
XX
PR 01-OCT-1998; 98US-0165042.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Sturley SL, Oelkers P;
XX
DR WPI; 2000-557622/51.
XX
PT New nucleic acid encoding a human diacylglycerol acyltransferase,
PT useful for treating hyperlipidemia, atherosclerosis, heart disease, or
PT other diseases associated with an imbalance of triglyceride levels -
XX
PS Disclosure; Column 17; 32pp; English.
XX

XX The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1)
XX mediates sterol esterification, an important component of intracellular
XX lipid homeostasis. The present invention relates to human ACAT Related
XX Gene Product 2 (ARGP2). ARGP2 is a diacylglycerol acyltransferase
XX (DGAT). ARGP2 is a tissue specific sterol esterification enzyme. The
XX present sequence is a PCR primer used to isolate ARGP2 coding sequence
XX (see AAA76170).

XX Sequence 23 BP; 3 A; 9 C; 5 G; 6 T; 0 other;

Query Match 1.5%; Score 23; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1539 GACACCTCGATCTTGCTCTGCC 1561
 |||||
 Db 1 GACACCTCGATCTTGCTCTGCC 23

RESULT 4

AAZ57363

ID AAZ57363 standard; DNA; 20 BP.

XX

AC AAZ57363;

XX

DT 05-APR-2000 (first entry)

XX

XX Human acyl CoA:cholesterol acyltransferase 2 sense PCR primer.

XX

KW Human; acyl CoA:cholesterol acyltransferase; ACAT-2; diagnosis;

KW

KW antilipaemic; hypercholesterolaemia; hypertriglyceridaemia;

KW

KW hyperlipidaemia; PCR primer; ss.

XX

OS Homo sapiens.

XX

XX WO9567368-A1.

XX

XX 29-DEC-1999.

XX

XX 16-JUN-1999; 99WO-US13683.

XX

XX 23-JUN-1998; 98US-0090354.

XX

XX 08-JUN-1999; 99US-0328857.

XX

XX (REGC) UNIV CALIFORNIA.

XX

XX Cases S, Farese RV, Novak S, Erickson SK;

XX

XX WPI; 2000-106291/09.

XX

XX Novel polypeptide, useful to treat conditions associated with elevated

XX

XX cholesterol ester levels e.g. hypercholesterolemia

XX

XX Example; Page 40; 57pp; English.

XX

XX The present sequence represents a PCR primer for the human acyl

XX

XX CoA:cholesterol acyltransferase designated ACAT-2. ACAT-2 polypeptides

XX

XX can be administered therapeutically, especially by expressing encoding

XX

XX polynucleotides, to treat individuals in need of ACAT-2 polypeptide.

XX

XX They may especially be administered to treat disease conditions

XX

XX associated with elevated cholesterol ester levels e.g.

XX

XX hypercholesterolaemia or hyperlipidaemia (including

XX

XX hypertriglyceridaemia), since ACAT-2 catalyses the esterification of

XX

XX cholesterol with fatty acyl CoA substrates. The polypeptides can also

XX

XX be used to diagnose diseases related to polypeptide expression or

XX

XX activity, by analysing for polypeptide presence or amount in a sample.

XX

XX They are useful to screen for compounds inhibiting or activating the

XX

XX polypeptide, which can be included in pharmaceutical compositions and

XX

XX administered therapeutically to treat conditions associated with ACAT-2;

XX

XX inhibitory agents can especially be used to inhibit ACAT-2 activity,

XX

XX especially therapeutically, and especially agents which selectively

XX

XX inhibit ACAT-2 and not prior art ACAT-1.

AAZ57364/c

ID AAZ57364 standard; DNA; 20 BP.

XX

AC AAZ57364;

XX

DT 05-APR-2000 (first entry)

XX

XX Human acyl CoA:cholesterol acyltransferase 2 antisense PCR primer.

XX

XX Human; acyl CoA:cholesterol acyltransferase; ACAT-2; diagnosis;

KW

KW antilipaemic; hypercholesterolaemia; hypertriglyceridaemia;

KW

KW hyperlipidaemia; PCR primer; ss.

XX

OS Homo sapiens.

XX

XX WO9567368-A1.

XX

XX 29-DEC-1999.

XX

XX 16-JUN-1999; 99WO-US13683.

XX

XX 23-JUN-1998; 98US-0090354.

XX

XX 08-JUN-1999; 99US-0328857.

XX

XX (REGC) UNIV CALIFORNIA.

XX

XX Cases S, Farese RV, Novak S, Erickson SK;

XX

XX WPI; 2000-106291/09.

XX

XX Novel polypeptide, useful to treat conditions associated with elevated

XX

XX cholesterol ester levels e.g. hypercholesterolemia

XX

XX Example; Page 40; 57pp; English.

XX

XX The present sequence represents a PCR primer for the human acyl

XX

XX CoA:cholesterol acyltransferase designated ACAT-2. ACAT-2 polypeptides

XX

XX can be administered therapeutically, especially by expressing encoding

XX

XX polynucleotides, to treat individuals in need of ACAT-2 polypeptide.

XX

XX They may especially be administered to treat disease conditions

XX

XX associated with elevated cholesterol ester levels e.g.

XX

XX hypercholesterolaemia or hyperlipidaemia (including

XX

XX hypertriglyceridaemia), since ACAT-2 catalyses the esterification of

XX

XX cholesterol with fatty acyl CoA substrates. The polypeptides can also

XX

XX be used to diagnose diseases related to polypeptide expression or

XX

XX activity, by analysing for polypeptide presence or amount in a sample.

XX

XX They are useful to screen for compounds inhibiting or activating the

XX

XX polypeptide, which can be included in pharmaceutical compositions and

XX

XX administered therapeutically to treat conditions associated with ACAT-2;

XX

XX inhibitory agents can especially be used to inhibit ACAT-2 activity,

XX

XX especially therapeutically, and especially agents which selectively

XX

XX inhibit ACAT-2 and not prior art ACAT-1.

XX

SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 other;

SQ

Query Match 1.3%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1418 GGAACGTGCTGATGGACC 1437

|||||

Db 20 GGAACGTGCTGATGGACC 1

RESULT 6

ABN28762

ID ABN28762 standard; DNA; 65 BP.

XX

AC ABN28762;

XX

DT 15-JUL-2002 (first entry)

XX

XX Rat spliced transcript detection oligonucleotide SEQ ID NO:1510.

XX

```
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Rattus norvegicus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes.
XX
XX Example 1; SEQ ID 1510; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 65 BP; 17 A; 24 C; 8 G; 16 T; 0 other;
SQ
Query Match 1.1%; Score 17; DB 24; Length 65;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 362 GCACCATCTACCATG 378
DB 48 GCACCATCTACCATG 64
RESULT 7
AAZ77373
ID AAZ77373 standard; DNA; 20 BP.
XX
XX AAZ77373;
AC
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:11729.
```

```
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 9; Page 2731; 2745pp; English.
XX
XX AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses; they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
XX Sequence 20 BP; 2 A; 10 C; 1 G; 7 T; 0 other;
SQ
Query Match 1.0%; Score 16; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 821 TCCTCTCTGCCCCAAC 836
DB 3 TCCTCTCTGCCCCAAC 18
RESULT 8
AAV21372
ID AAV21372 standard; DNA; 60 BP.
XX
XX AC AAV21372;
XX
XX 14-AUG-1998 (first entry)
XX
XX Immunoglobulin genomic I gamma 4-S gamma 4 junction.
XX
XX ss; Ig; heavy chain; stimulation; inhibition; treatment; IgM; IgG; IgA;
KW IgE; isotype switching; allergy; autoimmune; alloimmune.
XX
XX Homo sapiens.
XX
XX WO9807738-A1.
PN
```

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XX PD 26-FEB-1998.
XX PF
XX PF 15-AUG-1997; 97WO-US15485.
XX PR 19-AUG-1996; 96US-0023579.
XX PA (RECC ) UNIV CALIFORNIA.
XX FU Fujieda S, Ke Z, Saxon AW;
XX WI WPI; 1998-179050/16.
XX PT New immunoglobulin trans-spliced transcripts - used for, e.g.
XX PT stimulating or inhibiting synthesis of particular immunoglobulin
XX PT isotype, useful for treating immune disorders
XX PS Example 2; Page 36; 83pp; English.
XX CC The nucleotides AAV21362-V21373 are examples of the genomic fragments
XX CC from which sequences were used to create trans-spliced transcripts. The
XX CC transcripts comprise a sequence capable of annealing to a human genomic
XX CC immunoglobulin (Ig) heavy chain I region of a locus selected from mu,
XX CC epsilon, alpha and gamma followed by a second sequence capable of
XX CC annealing to a region of a second locus selected from mu, epsilon, alpha
XX CC and gamma as above. The products can be used for stimulating or
XX CC inhibiting synthesis of a particular human Ig isotype. They can be used
XX CC for treating disorders mediated by IgM, IgG, IgA or IgE, in particular
XX CC for inhibiting IgE synthesis or isotype switching to IgE for treating
XX CC allergic disorders. They can also be used for treating autoimmune and
XX CC alloimmune diseases amongst others.
XX SQ Sequence 60 BP; 16 A; 8 C; 30 G; 6 T; 0 other;
Query Match 1.0%; Score 16; DB 19; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 GCAGAGGACAGAGG 45
DB 40 GCAGAGGACAGAGG 55
|||||
RESULT 9
ABA50541
ID ABA50541 standard; DNA; 87 BP.
XX AC ABA50541;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #9236.
XX KW Human; microarray; single exon probe; gene expression; breast;
XX KW disease; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00662.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
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XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes,
XX PT useful for measuring gene expression in sample derived from human
XX PT breast, comprises number of single exon nucleic acid probes -
XX PS Claim 4; SEQ ID NO 9236; 327pp + sequence listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and BT 474 cells. The method involves contacting
XX CC the probes with a collection of detectably labelled nucleic acids
XX CC derived from mRNA of human breast, and then measuring the label
XX CC bound to each probe of the microarray. The probes are useful for
XX CC verifying the expression of regions of genomic DNA predicted to
XX CC encode proteins. They are useful for gene discovery, and for
XX CC determining predisposition and/or prognosing breast disease. Gene
XX CC expression analysis is useful for assessing the toxicity of chemical
XX CC agents on cells. The microarray of this invention presents a far greater
XX CC diversity of probes for measuring gene expression, with far less bias
XX CC than expressed sequence tag microarrays. The method is suitable for
XX CC rapid production of functional information from genomic sequence. The
XX CC present sequence is a single exon nucleic acid probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
Query Match 1.0%; Score 16; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 134 TGGAGGCTGTGAAGC 149
DB 5 TGGAGGCTGTGAAGC 20
|||||
RESULT 10
ABA68500
ID ABA68500 standard; DNA; 87 BP.
XX AC ABA68500;
XX DT 01-FEB-2002 (first entry)
XX DE Human foetal liver single exon nucleic acid probe #16805.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX OS Homo sapiens.
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00669.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
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DR WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
PS Claim 4; SEQ ID NO 16805; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
Query Match 1.0%; Score 16; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 134 TGGAGGCTGTGAAGGC 149
Db 5 TGGAGGCTGTGAAGGC 20
RESULT 11
ABA35481
ID ABA35481 standard; DNA; 87 BP.
AC ABA35481;
XX
DT 23-JAN-2002 (first entry)
DE Probe #13947 for gene expression analysis in human heart cell sample.
XX
XX Human: gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 4; SEQ ID No 13947; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived

CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
Query Match 1.0%; Score 16; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 134 TGGAGGCTGTGAAGGC 149
Db 5 TGGAGGCTGTGAAGGC 20
RESULT 12
AAK16867
ID AAK16867 standard; DNA; 87 BP.
AC AAK16867;
XX
DT 05-NOV-2001 (first entry)
DE Human brain expressed single exon probe SEQ ID NO: 16858.
XX
XX Human: brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 16858; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
Query Match 1.0%; Score 16; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;

```
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 134 TGGAGGCTGTGAAGGC 149
Db 5 TGGAGGCTGTGAAGGC 20

RESULT 13
AAK42636
ID AAK42636 standard; DNA; 87 BP.
XX
AC AAK42636;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 17193.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 17193; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;

Query Match 1.0%; Score 16; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 134 TGGAGGCTGTGAAGGC 149
Db 5 TGGAGGCTGTGAAGGC 20

RESULT 14
AAI23392
ID AAI23392 standard; DNA; 87 BP.
XX
AC AAI23392;
XX
DT 12-OCT-2001 (first entry)
XX
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```
DE Probe #13325 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID NO 13325; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;

Query Match 1.0%; Score 16; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 134 TGGAGGCTGTGAAGGC 149
Db 5 TGGAGGCTGTGAAGGC 20

RESULT 15
AAI48715
ID AAI48715 standard; DNA; 87 BP.
XX
AC AAI48715;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #17401 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
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PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID NO 17401; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 87 Bp; 25 A; 17 C; 28 G; 17 T; 0 other;

Query Match      1.0%; Score 16; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TGGAGGCTGTGAAGGC 149
Db      |||||
        5 TGGAGGCTGTGAAGGC 20

Search completed: November 14, 2002, 19:34:47
Job time : 256 secs

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 20801
 ; LENGTH: 87
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AL022308.1
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.5
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.6
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.5
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.4
 ; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 8.4
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.4
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.7
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.4
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.7
 ; OTHER INFORMATION: NT HIT: U91328.1, EVALUE 1.00e-11
 ; OTHER INFORMATION: SWISSPROT HIT: P80152, EVALUE 7.10e+00
 ; OTHER INFORMATION: EST_HUMAN HIT: R09942.1, EVALUE 1.00e-17
 ; US-09-864-761-20801

Query Match 1.0%; Score 16; DB 10; Length 87;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TGGAGGCTGTGAAGGC 149
 |||||
 DB 5 TGGAGGCTGTGAAGGC 20

RESULT 2
 US-09-854-883-174/c
 ; Sequence 174, Application US/09854883
 ; Patent No. US20020055479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lex M. Cowser
 ; APPLICANT: Jacqueline Wyatt
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Madeline M. Butler
 ; APPLICANT: Robert McKay
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPIB EXPRESSION
 ; FILE REFERENCE: ISPH-0576
 ; CURRENT APPLICATION NUMBER: US/09/854,883
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: US 09/629,644
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US 09/487,368
 ; PRIOR FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 389
 ; SEQ ID NO 174
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 ; US-09-854-883-174

Query Match 1.0%; Score 15; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 TGCCCCCACCTCCCC 259

DB 20 TGCCCCCACCTCCCC 6
 |||||

RESULT 3
 US-09-775-925-16/c
 ; Sequence 16, Application US/09775925
 ; Patent No. US20010049358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Luche, Ralf M.
 ; APPLICANT: Wei, Bo
 ; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
 ; TITLE OF INVENTION: PHOSPHATASES
 ; FILE REFERENCE: 200125.420
 ; CURRENT APPLICATION NUMBER: US/09/775,925
 ; CURRENT FILING DATE: 2001-02-01
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 ; US-09-775-925-16

Query Match 1.0%; Score 15; DB 10; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 CTGCCCCACCTCCC 258
 |||||
 DB 22 CTGCCCCACCTCCC 8

RESULT 4
 US-09-801-274-4/c
 ; Sequence 4, Application US/09801274
 ; Patent No. US20020032319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cargill, Michele
 ; APPLICANT: Ireland, James S.
 ; APPLICANT: Lander, Eric S.
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 ; FILE REFERENCE: 2825.2009-001
 ; CURRENT APPLICATION NUMBER: US/09/801,274
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/187,510
 ; PRIOR FILING DATE: 2000-03-07
 ; PRIOR APPLICATION NUMBER: US 60/206,129
 ; PRIOR FILING DATE: 2000-05-22
 ; NUMBER OF SEQ ID NOS: 1802
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 31
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-801-274-4

Query Match 1.0%; Score 15; DB 10; Length 31;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CTGGGTGCCCATGT 520
 |||||
 DB 31 CTGGGTGCCCATGT 17

RESULT 5
 US-09-898-323-20
 ; Sequence 20, Application US/09898323
 ; Patent No. US20020150904A1
 ; GENERAL INFORMATION:

APPLICANT: Bl, Wanli
APPLICANT: Livak, Kenneth J.
APPLICANT: Bloch, Will
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE ASSAY
FILE REFERENCE: 4559US
CURRENT APPLICATION NUMBER: US/09/898,323
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/216,514
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 51
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Complement of SEQ ID NO:2
US-09-898-323-20

Query Match 1.0%; Score 15; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 819 CTTCTCTTCTGCC 833
|||||

DB 36 CTTCTCTTCTGCC 50

RESULT 6
US-09-919-060-25/c
Sequence 25, Application US/09919060
Patent No. US20020064845A1
GENERAL INFORMATION:
APPLICANT: Wisniewski, Nancy
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
FILE REFERENCE: AD-1
CURRENT APPLICATION NUMBER: US/09/919,060
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/224,486
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Primer
US-09-919-060-25

Query Match 0.9%; Score 14; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 GGCTGTGGCCAGG 570
|||||

DB 22 GGCTGTGGCCAGG 9

RESULT 7
US-09-292-973-8
Sequence 8, Application US/09292973
Patent No. US2002011473A1
GENERAL INFORMATION:
APPLICANT: ZASTAWNY, Roman L.
APPLICANT: MCWHINNIE, Elizabeth A.
TITLE OF INVENTION: NO. US2002011473A1e1 G Protein Coupled Receptor
FILE REFERENCE: 8074-9004
CURRENT APPLICATION NUMBER: US/09/292,973
CURRENT FILING DATE: 1999-04-16
EARLIER APPLICATION NUMBER: US 60/081,995
EARLIER FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-292-973-8

Query Match 0.9%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1049 TGCTGCTGCTCATC 1062
|||||

DB 6 TGCTGCTGCTCATC 19

RESULT 8
US-09-898-541-18/c
Sequence 18, Application US/09898541
Patent No. US20020072504A1
GENERAL INFORMATION:
APPLICANT: Houghton, Alan
Bartido, Shirley M.
Xu, Yiquing
Wang, Siqun
TITLE OF INVENTION: Method and Reagents for Genetic Immunization
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: PO Box 5270
CITY: Frisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,541
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: MSK.P-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2082
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
SEQUENCE DESCRIPTION: SEQ ID NO: 18
US-09-898-541-18

Query Match 0.9%; Score 14; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Nov 15 09:17:47 2002

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QY 763 CTTGTCGCCAGCG 776
Db 15 CTTGTCGCCAGCG 2

RESULT 9
US-09-815-837-104
; Sequence 104, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Darrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Immune Mediators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:phosphorylated
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: n = 5' phosphorylated c
US-09-815-837-104

Query Match 0.9%; Score 14; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 612 AGCGGCCCGCGCG 625
Db 13 AGCGGCCCGCGCG 26

RESULT 10
US-09-785-632A-6/C
; Sequence 6, Application US/09785632A
; Patent No. US20020061512A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Kwon, Young Do
; APPLICANT: Kim, Hyun-Won
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAINS AND METHODS OF
; FILE REFERENCE: 12279-002001
; CURRENT APPLICATION NUMBER: US/09/785,632A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: optimal binding site
US-09-785-632A-6

Query Match 0.9%; Score 14; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 612 AGCGGCCCGCGCG 625
Db 15 AGCGGCCCGCGCG 2

RESULT 11
US-09-898-323-24
; Sequence 24, Application US/09898323
; Patent No. US20020150904A1
; GENERAL INFORMATION:
; APPLICANT: Bi, Wanli
; APPLICANT: Livak, Kenneth J.
; APPLICANT: Bloch, Will
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE ASSAY
; FILE REFERENCE: 4559US
; CURRENT APPLICATION NUMBER: US/09/898,323
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/216,514
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Ligation product of probes Ap3 and Ap4 from Scheme I1b, follow
; OTHER INFORMATION: cleavage of Ap4
US-09-898-323-24

Query Match 0.9%; Score 14; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 819 CTTCTCTCTCTGCG 832
Db 32 CTTCTCTCTCTGCG 45

RESULT 12
US-09-878-574-3227
; Sequence 3227, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3227
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-C8
US-09-878-574-3227

Query Match 0.9%; Score 14; DB 10; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1267 ATGCTGGGTGTGT 1280
Db 1267 ATGCTGGGTGTGT 1280
```

Db 27 ATGCTGGCTGTGT 40

RESULT 13

US-09-864-761-24518

; Sequence 24518, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aecmica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1

; SEQ ID NO 24518

; LENGTH: 82

; TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AL162260.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

OTHER INFORMATION: EST_HUMAN HIT: AW581997.1, EVALUE 2.50e-01

US-09-864-761-24518

Query Match

0.9%; Score 14; DB 10; Length 82;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 GTGGAGATGGAAC 87

|||||

Db 32 GTGGAGATGGAAC 45

RESULT 14

US-09-920-300A-1141/c

; Sequence 1141, Application US/09920300A

; Patent No. US20020136728A1

; GENERAL INFORMATION:

; APPLICANT: King, Gordon E.

; APPLICANT: Meagher, Madeleine Joy

; APPLICANT: Xu, Jiangchun

; APPLICANT: Secrist, Heather

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.547

; CURRENT APPLICATION NUMBER: US/09/920,300A

; CURRENT FILING DATE: 2001-07-31

; NUMBER OF SEQ ID NOS: 1789

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1141

; LENGTH: 88

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-920-300A-1141

Query Match 0.9%; Score 14; DB 10; Length 88;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 384 CGCTGGCCTGTGTG 397

|||||

Db 29 CGCTGGCCTGTGTG 16

RESULT 15

US-10-033-528-1141/c

; Sequence 1141, Application US/10033528

; Patent No. US20020131971A1

; GENERAL INFORMATION:

; APPLICANT: King, Gordon E.

; APPLICANT: Meagher, Madeleine Joy

; APPLICANT: Xu, Jiangchun

; APPLICANT: Secrist, Heather

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.547C1

; CURRENT APPLICATION NUMBER: US/10/033,528

; CURRENT FILING DATE: 2001-12-26

; NUMBER OF SEQ ID NOS: 1896

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1141

; LENGTH: 88

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-033-528-1141

Query Match 0.9%; Score 14; DB 12; Length 88;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 384 CGCTGGCCTGTGTG 397

|||||

Db 29 CGCTGGCCTGTGTG 16

Search completed: November 14, 2002, 20:57:26

Job time : 73 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 19:27:46 ; Search time 1868 Seconds
(without alignments)
13603.168 Million cell updates/sec

Title: US-09-918-026A-3
Perfect score: 1569
Sequence: 1 atggagccaggcgggccg.....cttggtctgccatacctag 1569

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0
Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_Other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	1.1	71	17 AZ920873	AZ920873 1006021F0
2	17	1.1	80	14 F31995	F31995 HSPD23742 H
3	17	1.1	89	13 BI472373	BI472373 fs02d01.y
4	17	1.1	91	9 AA791480	AA791480 vs66f11.r
5	17	1.1	93	14 F24292	F24292 HSPD10465 H
6	16	1.0	74	17 BH850932	BH850932 SALK_0721

c	7	16	1.0	76	17	AZ783832
c	8	16	1.0	88	17	BH417282
c	9	16	1.0	91	17	B39146
c	10	16	1.0	100	13	BI175453
c	11	15	1.0	36	17	AZ492139
c	12	15	1.0	50	9	AU105499
c	13	15	1.0	50	9	AU105500
c	14	15	1.0	50	9	AU105502
c	15	15	1.0	50	9	AU105503
c	16	15	1.0	55	9	A1828950
c	17	15	1.0	55	17	AZ389723
c	18	15	1.0	58	10	BE041235
c	19	15	1.0	58	10	BE043557
c	20	15	1.0	70	10	BE043227
c	21	15	1.0	70	10	BE043859
c	22	15	1.0	71	9	A1223516
c	23	15	1.0	72	10	BE042163
c	24	15	1.0	72	10	BE043435
c	25	15	1.0	73	10	BE043561
c	26	15	1.0	73	9	A1223491
c	27	15	1.0	75	13	BI676290
c	28	15	1.0	75	14	TI0503
c	29	15	1.0	76	9	A1197018
c	30	15	1.0	76	10	BE043899
c	31	15	1.0	77	10	BE043552
c	32	15	1.0	78	10	BE043531
c	33	15	1.0	79	12	BF055887
c	34	15	1.0	81	9	A1242007
c	35	15	1.0	81	9	A1307038
c	36	15	1.0	81	9	A1324831
c	37	15	1.0	83	9	A1224332
c	38	15	1.0	83	9	A1336711
c	39	15	1.0	83	9	A1337638
c	40	15	1.0	83	9	A1340813
c	41	15	1.0	84	9	A1249840
c	42	15	1.0	84	9	A1250328
c	43	15	1.0	84	9	A1250596
c	44	15	1.0	84	9	A1270886
c	45	15	1.0	84	9	A1271125

ALIGNMENTS

RESULT 1
AZ920873
LOCUS 1006021F08.xl 1006 - RescueMu Grid G Zea mays genomic, DNA
DEFINITION 71 bp linear
ACCESSION AZ920873
VERSION AZ920873.1 GI:13391744
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE 1 (bases 1 to 71)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by a single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006021 row: 38
Class: transposon-tagged.
Location/Qualifiers

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 71)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by a single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006021 row: 38
Class: transposon-tagged.
Location/Qualifiers

```

source
1. .71
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu'. Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
BASE COUNT      7 a   27 c   16 g   21 t
ORIGIN
Query Match      1.1%; Score 17; DB 17; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1043 TCTTCATGCTGCTGCTC 1059
|||||
Db 34 TCTTCATGCTGCTGCTC 50

RESULT 2
F31995/c
LOCUS      HSPD23742 HM3 Homo sapiens cDNA clone s400089G03, mRNA sequence.
DEFINITION F31995
VERSION    F31995.1 GI:4817621
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80)
REFERENCE  1 (bases 1 to 80)
AUTHORS   Lanfranchi, G., Muraro, T., Caldarà, F., Pacchioni, B., Pallavicini, A.,
Pantolito, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.
TITLE     Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
JOURNAL   Genome Res. 6 (1), 35-42 (1996)
MEDLINE   96276048
COMMENT   Contact: Valle G.
          CRIBI Biotechnology Centre
          University of Padua
          Via Trieste 75, 35121 Padua, Italy
          ABI Chromatograms and other information are available on WWW at
          http://grup.bio.unipd.it.
          Location/Qualifiers
            1..80
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="s400089G03"
              /clone_lib="HM3"
              /sex="female"
              /tissue_type="pectoral muscle (after mastectomy)"
              /note="Vector: pCDNAII (Invitrogen); Site_1: BstXI;
              Site_2: NotI; The library is not subtracted nor normalized.
              The first strand cDNA was primed with a biotinylated
              oligo-dT-NotI primer
              (5'-biotin-AACCGGCTGAGCGCGCTTTTCTTTTCTTTTCTTTT-3'). The
              ds cDNA was sonicated and size-selected in the range
              350-550 bp. The 3' specific fragments were selected by

```

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streptavidin coated magnetic beads, ligated to
non-palindromic BstXI adapters, NotI digested and
directionally cloned into BstXI-NotI cut pCDNAII vector."
BASE COUNT      25 a   20 c   25 g   10 t
ORIGIN
Query Match      1.1%; Score 17; DB 14; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 438 GGCAGGCTGCTGCTGG 454
|||||
Db 56 GGCAGGCTGCTGCTGG 40

RESULT 3
BI472373
LOCUS      fs02d01.y1 zebrafish adult olfactory Danio rerio cDNA clone 5002416
DEFINITION BI472373
VERSION    BI472373.1 GI:15288482
KEYWORDS   EST.
SOURCE     zebrafish.
ORGANISM   Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 89)
REFERENCE  1 (bases 1 to 89)
AUTHORS   Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
TITLE     WASNU Zebrafish EST Project 1998
JOURNAL   Unpublished (1998)
COMMENT   Contact: Stephen L. Johnson
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: zbrafish@watson.wustl.edu
          cDNA Library Preparation: John Ngai cDNA Library Arrayed by:
          Matthew Clark. DNA Sequencing By: Washington University Genome
          Sequencing Center Clone distribution: Genome Systems, St. Louis,
          Missouri (web address: www.genomesystems.com) (email contact:
          info@genomesystems.com) and Research Genetics, Huntsville, Alabama
          (web address: www.resgen.com) (email contact: info@resgen.com) and
          RessourcenzentrumPrimatendatenbank, Berlin, Germany (web address:
          www.rzpd.de).
          Location/Qualifiers
            1..89
              /organism="Danio rerio"
              /db_xref="taxon:7955"
              /clone="5002416"
              /clone_lib="zebrafish adult olfactory"
              /sex="mixed"
              /tissue_type="Olfactory rosettes"
              /dev_stage="adult"
              /lab_host="D10Hb (Gibco BRL)"
              /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This
              is a directionally cloned cDNA library from adult
              zebrafish olfactory epithelium."
BASE COUNT      26 a   21 c   25 g   17 t
ORIGIN
Query Match      1.1%; Score 17; DB 13; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 132 CATGGAGCTGTGAAGG 148
|||||

```

Db 62 CATGGAGGCTGTGAAGG 78

RESULT 4
AA791480
LOCUS
DEFINITION VS66f11.r1 Strata gene mouse skin (#937313) Mus musculus cDNA clone
VERSION AA791480
KEYWORDS EST.
SOURCE AA791480.1 GI:2854435
ORGANISM house mouse.
REFERENCE Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 91)
Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Willson, R. and Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:624485
Seq primer: -28ml3 rev1 ET from Amersham.

FEATURES
Location/Qualifiers
1..91
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1151277"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site.1: EcoRI ; Site.2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGTGT 3' "

BASE COUNT 18 a 22 c 21 g 30 t

ORIGIN
Query Match 1.1%; Score 17; DB 9; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 919 TCTGTGCTCTATGCTGTG 935
|||||
Db 74 TCTGTGCTCTATGCTGTG 90

RESULT 5
F24292/c
LOCUS F24292
DEFINITION HSPD10465 HM3 Homo sapiens cDNA clone s400006H09, mRNA sequence.
VERSION F24292
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 93)
Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.
Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
Genome Res. 6 (1), 35-42 (1996)
96276048
Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
http://grup.bio.unipd.it.

FEATURES
Location/Qualifiers
1..93
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s400006H09"
/clone_lib="HM3"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pCDNall (Invitrogen); Site.1: BstXI; Site.2: NotI; The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer
(5'-biotin-AACCGCTGCGAGCGCGCGCTTTT-3'). The ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pCDNall vector."

BASE COUNT 29 a 27 c 26 g 11 t

ORIGIN
Query Match 1.1%; Score 17; DB 14; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 438 GGGCAGGCTGTGCTGG 454
|||||
Db 48 GGGCAGGCTGTGCTGG 32

RESULT 6
BH850932/c
LOCUS
DEFINITION BH850932 74 bp DNA linear GSS 13-JUN-2002
Arabidopsis thaliana genomic clone SALK_072110.31.45.x, DNA sequence.

ACCESSION BH850932
VERSION BH850932.1 GI:21421803
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1 (bases 1 to 74)
Alonso, J.M., Leisbe, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At3g54900.
Class: TDNA tagged.

FEATURES

Location/Qualifiers

1. .74
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_072110.31.45.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 22 a 20 c 17 g 15 t
ORIGIN
Query Match 1.0%; Score 16; DB 17; Length 74;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 795 CCCAGTTTCTCCAGC 810
|||||
Db 70 CCCAGTTTCTCCAGC 55

RESULT 7

AZ783832/c
LOCUS
DEFINITION
2M0025B16R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0025B16 R, DNA sequence.

ACCESSION
A2783832
VERSION
A2783832.1
KEYWORDS
GSS.
SOURCE
house mouse.

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 76)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: B column: 16
Seq primer: CACACAGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 76.
Location/Qualifiers
1. .76
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0025B16"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 16 a 18 c 29 g 13 t
ORIGIN
Query Match 1.0%; Score 16; DB 17; Length 76;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 GGCTGCTGCTGGAGTT 458
|||||
Db 21 GGCTGCTGCTGGAGTT 6

RESULT 8

BH417282
LOCUS
DEFINITION
1007053G01.y1 1007 - RescueMu Grid H Zea mays genomic, DNA
sequence.

ACCESSION
BH417282
VERSION
BH417282.1
KEYWORDS
GSS.
SOURCE
Zea mays.

ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 88)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007053 column: 17
Class: transposon-tagged.
Location/Qualifiers
1. .88
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1007 - RescueMu Grid H"
/dev_stage="adult"
/tissue_type="leaf"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site.1: BamHI; Site.2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for

FEATURES

source
Location/Qualifiers
1. .88
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1007 - RescueMu Grid H"
/dev_stage="adult"
/tissue_type="leaf"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site.1: BamHI; Site.2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin." 14 t

BASE COUNT 13 a 23 c 38 g 14 t
ORIGIN

Query Match 1.0%; Score 16; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTTGATGAGCTGATGG 346
|||||
Db 61 CTTGATGAGCTGATGG 76

RESULT 9
LOCUS B39146 91 bp DNA linear GSS 18-OCT-1997
DEFINITION HS-1049-A1-F09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=17 Row=K, DNA sequence.

ACCESSION B39146
VERSION B39146.1 GI:2543398
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 91)
AUTHORS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.

TITLE Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors
JOURNAL Unpublished (1997)

COMMENT Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 771 row: K column: 17
Class: BAC ends
High quality sequence stop: 91.

FEATURES Location/Qualifiers
1..91

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate=CT 771 Col=17 Row=K"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 21 a 20 c 16 g 34 t
ORIGIN
Query Match 1.0%; Score 16; DB 17; Length 91;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1380 GAACTTCATGATGCAT 1395
|||||
Db 39 GAACTTCATGATGCAT 24

RESULT 10
LOCUS B1175453 100 bp mRNA linear EST 09-JUL-2001
DEFINITION OSTR04645_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to T205.8, mRNA sequence.
ACCESSION B1175453

VERSION B1175453.1 GI:14641256
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderiinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 100)
AUTHORS Rebol,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T., Jackson,C., Shin-I,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J., Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F., Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

JOURNAL 21135099
MEDLINE
COMMENT Contact: Rebol J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425

Email: Jerome.Rebol@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact Jerome_rebol@dfci.harvard.edu or philippe_vaglio@dfci.harvard.edu
POLYA=No.

FEATURES Location/Qualifiers
1..100

/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="AD-wrmcDNA"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pCR86"

BASE COUNT 30 a 22 c 26 g 22 t
ORIGIN
Query Match 1.0%; Score 16; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 TCTTCATCATCAGCAC 413
|||||
Db 62 TCTTCATCATCAGCAC 77

RESULT 11
AZ492139/c
LOCUS 36 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0326005F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0326005 F, DNA sequence.

ACCESSION AZ492139
VERSION AZ492139.1 GI:10664562
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 36)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

```

COMMENT      Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0326 row: 0 column: 05
              Seq primer: CCGTGTAAACGACGGCCAGT
              Class: plasmid ends
              High quality sequence stop: 36.
FEATURES     Location/Qualifiers
             1..36
             /organism="Mus musculus"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC1M0326005"
             /clone_lib="Mouse 10kb plasmid UUGC1M library"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of PWD42 (gi14732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid RL. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
BASE COUNT   9 a 6 c 13 g 8 t
ORIGIN
Query Match 1.0%; Score 15; DB 17; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 952 CTCTGTGTTCTGTGTC 966
|||||
Db 34 CTCTGTGTTCTGTGTC 20

RESULT 12
LOCUS AU105499/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU105499 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC07611, mRNA sequence.
ACCESSION AU105499
VERSION AU105499.1 GI:13555020
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES     Location/Qualifiers
             1..50
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="HRC07611"
             /clone_lib="Sugano Homo sapiens cDNA library"
             /note="Differential display comparison of untreated and
             dimethylfumarate treated U937 cells"
BASE COUNT   11 a 12 c 18 g 9 t
ORIGIN
Query Match 1.0%; Score 15; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 TCCTGGTCTCCGCAG 1294
|||||
Db 28 TCCTGGTCTCCGCAG 14

RESULT 13
LOCUS AU105500/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU105500 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC12477, mRNA sequence.
ACCESSION AU105500
VERSION AU105500.1 GI:13555021
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES     Location/Qualifiers
             1..50
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="HRC12477"
             /clone_lib="Sugano Homo sapiens cDNA library"
             /note="Differential display comparison of untreated and
             dimethylfumarate treated U937 cells"
BASE COUNT   13 a 12 c 18 g 7 t
ORIGIN
Query Match 1.0%; Score 15; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 TCCTGGTCTCCGCAG 1294
|||||

```

```

Db 30 TCCTGGTCTCCGCAG 16

RESULT 14
LOCUS AU105502/c
DEFINITION AU105502 Sugano Homo sapiens cDNA library EST 30-AUG-2001
KAT00658, mRNA sequence.
ACCESSION AU105502
VERSION AU105502.1 GI:13555023
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KAT04851"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylformate treated U937 cells"
BASE COUNT 11 a 13 c 18 g 8 t
ORIGIN
11 a 13 c 18 g 8 t
Query Match 1.0%; Score 15; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 TCCTGGTCTCCGCAG 1294
|||||
Db 27 TCCTGGTCTCCGCAG 13

Search completed: November 14, 2002, 20:54:33
Job time : 1871 secs

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KAT04851"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylformate treated U937 cells"
BASE COUNT 11 a 13 c 18 g 8 t
ORIGIN
11 a 13 c 18 g 8 t
Query Match 1.0%; Score 15; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 TCCTGGTCTCCGCAG 1294
|||||
Db 27 TCCTGGTCTCCGCAG 13

Search completed: November 14, 2002, 20:54:33
Job time : 1871 secs

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KAT00658"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylformate treated U937 cells"
BASE COUNT 11 a 14 c 19 g 6 t
ORIGIN
11 a 14 c 19 g 6 t
Query Match 1.0%; Score 15; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 TCCTGGTCTCCGCAG 1294
|||||
Db 26 TCCTGGTCTCCGCAG 12

RESULT 15
LOCUS AU105503/c
DEFINITION AU105503 Sugano Homo sapiens cDNA library EST 30-AUG-2001
KAT04851, mRNA sequence.
ACCESSION AU105503
VERSION AU105503.1 GI:13555024
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 19:30:01 ; Search time 61 Seconds
(without alignments)
7888.129 Million cell updates/sec

Title: US-09-918-026A-3
Perfect score: 1569
Sequence: 1 atggagcagcgggggccg.....cttggctcgcatacctag 1569

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	1.5	25	US-09-165-042-25	Sequence 25, Appl
2	23	1.5	23	US-09-165-042-30	Sequence 30, Appl
3	16	1.0	60	US-08-911-894-67	Sequence 67, Appl
4	16	1.0	89	US-08-974-549A-683	Sequence 683, Appl
5	16	1.0	90	US-08-974-549A-684	Sequence 684, Appl
6	15	1.0	17	US-08-985-162-144	Sequence 144, Appl
7	15	1.0	20	US-09-487-368A-174	Sequence 174, Appl
8	15	1.0	20	US-09-676-610B-171	Sequence 171, Appl
9	15	1.0	76	US-08-482-182-37	Sequence 37, Appl
10	15	1.0	80	US-08-482-182-36	Sequence 36, Appl
11	14	0.9	18	US-08-411-796-283	Sequence 283, Appl
12	14	0.9	18	US-08-471-039-283	Sequence 283, Appl
13	14	0.9	18	US-08-584-040-4455	Sequence 4455, Ap
14	14	0.9	18	PCT-US93-11198-283	Sequence 283, Appl
15	14	0.9	20	US-09-851-520-54	Sequence 54, Appl
16	14	0.9	21	US-08-940-968-2	Sequence 2, Appl
17	14	0.9	21	5455029-28	Patent No. 5455029
18	14	0.9	23	US-09-182-117-23	Sequence 23, Appl
19	14	0.9	24	US-08-890-980-84	Sequence 84, Appl
20	14	0.9	24	US-09-032-894-84	Sequence 84, Appl
21	14	0.9	24	US-09-031-626-84	Sequence 84, Appl
22	14	0.9	26	US-09-255-368-13	Sequence 13, Appl
23	14	0.9	27	US-08-411-796-282	Sequence 282, Appl
24	14	0.9	27	US-08-758-306-1166	Sequence 1166, Ap
25	14	0.9	27	US-08-471-039-282	Sequence 282, Appl
26	14	0.9	27	US-08-998-099-231	Sequence 231, Appl
27	14	0.9	27	US-09-417-822-19	Sequence 19, Appl

c 28	14	0.9	27	5	PCT-US93-11198-282	Sequence 282, App
c 29	14	0.9	27	6	5175384-4	Patent No. 5175384
c 30	14	0.9	30	3	US-08-996-338-36	Sequence 36, Appl
c 31	14	0.9	30	4	US-09-230-199-18	Sequence 18, Appl
c 32	14	0.9	30	6	5401629-1	Patent No. 5401629
c 33	14	0.9	31	4	US-08-679-645-286	Sequence 286, App
c 34	14	0.9	35	3	US-08-943-336A-15	Sequence 15, Appl
c 35	14	0.9	35	5	PCT-US95-01780-15	Sequence 15, Appl
c 36	14	0.9	36	1	US-08-363-240A-337	Sequence 337, App
c 37	14	0.9	36	1	US-08-363-240A-863	Sequence 863, App
c 38	14	0.9	36	1	US-08-363-240A-864	Sequence 864, App
c 39	14	0.9	36	1	US-08-363-240A-865	Sequence 865, App
c 40	14	0.9	36	3	US-08-891-516-48	Sequence 48, Appl
c 41	14	0.9	37	3	US-08-808-881-20	Sequence 20, Appl
c 42	14	0.9	37	3	US-09-017-631-20	Sequence 21, Appl
c 43	14	0.9	39	3	US-08-865-960-21	Sequence 66, Appl
c 44	14	0.9	39	4	US-08-993-674A-66	Sequence 66, Appl
c 45	14	0.9	39	4	US-09-256-976-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-165-042-25
; Sequence 25, Application US/09165042
; Patent No. 6100077
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.
; APPLICANT: Oelkers, Peter
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; TITLE OF INVENTION: ACYLTRANSFERASE
; FILE REFERENCE: 0575/56331
; CURRENT APPLICATION NUMBER: US/09/165,042
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 25
; TYPE: DNA
; ORGANISM: human
US-09-165-042-25

Query Match 1.5%; Score 24; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.052; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 1047 CATGCTGCTGCATCTCTCTTGC 1070
Db 1 CATGCTGCTGCATCTCTTGC 24

RESULT 2
US-09-165-042-30
; Sequence 30, Application US/09165042
; Patent No. 6100077
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.
; APPLICANT: Oelkers, Peter
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; TITLE OF INVENTION: ACYLTRANSFERASE
; FILE REFERENCE: 0575/56331
; CURRENT APPLICATION NUMBER: US/09/165,042
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 23
; TYPE: DNA
; ORGANISM: human
US-09-165-042-30

Query Match 1.5%; Score 23; DB 3; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

Qy 1539 GACACCTCGATCTTGCTGCTGCC 1561
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Db 1 GACACCTCGATCTTGCTGCTGCC 23

RESULT 3

US-08-911-894-67
; Sequence 67, Application US/08911894
; Patent No. 6030830
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Fujieda, Shigeharu
; TITLE OF INVENTION: IMMUNOGLOBULIN TRANS-SPLICED TRANSCRIPTS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld
; STREET: 816 Congress Avenue, Suite 1900
; CITY: Austin
; STATE: Texas
; COUNTRY: USA
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911.894
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,579
; FILING DATE: 19-AUG-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: 43496.0006
; TELEPHONE: (512) 499-6200
; TELEFAX: (512) 499-6290
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-911-894-67

Query Match 1.0%; Score 16; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 GCAGAGGACAGAGG 45
|||||
Db 40 GCAGAGGACAGAGG 55

RESULT 4

US-08-974-549A-683
; Sequence 683, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00261005
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 683:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..89
; OTHER INFORMATION: /note="oligonucleotide 21B"
US-08-974-549A-683

Query Match 1.0%; Score 16; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 CTTACGCTTCGGACAG 486
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Db 57 CTTACGCTTCGGACAG 72

RESULT 5

US-08-974-549A-684/c
; Sequence 684, Application US/08974549A
; Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morio, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 684:

SEQUENCE CHARACTERISTICS:
LENGTH: 90 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

NAME/KEY: -

LOCATION: 1..90

OTHER INFORMATION: /note= "oligonucleotide 21"

US-08-974-549A-684

Query Match 1.0%; Score 16; DB 4; Length 90;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 CTTACGCTTCGGACAG 486

|||||

Db 43 CTTACGCTTCGGACAG 28

RESULT 6

US-08-985-162-144/c

; Sequence 144, Application US/08985162

; Patent No. 6057156

GENERAL INFORMATION:

APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/985,162

FILING DATE: 04 December 1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/036,476

FILING DATE: 31 January 1997

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 230/107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 144:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-985-162-144

Query Match 1.0%; Score 15; DB 3; Length 17;

Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Gaps 0; Indels 0;

QY 340 CTGATGAGGTGCAG 354
 Db 15 CTGATGAGGTGCAG 1

RESULT 7
 US-09-487-368A-174/c
 ; Sequence 174, Application US/09487368A
 ; Patent No. 6261840
 ; GENERAL INFORMATION:
 ; APPLICANT: Lex M. Cowser
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPIB EXPRESSION
 ; FILE REFERENCE: RTS-0093
 ; CURRENT APPLICATION NUMBER: US/09/487,368A
 ; CURRENT FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 240
 ; SEQ ID NO 174
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-487-368A-174

Query Match 1.0%; Score 15; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Gaps 0; Indels 0;

QY 245 TGCCTCCACCTCCCC 259
 Db 20 TGCCTCCACCTCCCC 6

RESULT 8
 US-09-676-610B-171
 ; Sequence 171, Application US/09676610B
 ; Patent No. 644465
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Jacqueline Wyatt
 ; APPLICANT: Susan M. Freier
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
 ; FILE REFERENCE: RTS-0138
 ; CURRENT APPLICATION NUMBER: US/09/676,610B
 ; CURRENT FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 182
 ; SEQ ID NO 171
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-676-610B-171

Query Match 1.0%; Score 15; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Gaps 0; Indels 0;

QY 340 CTGATGAGGTGCAG 354
 Db 5 CTGATGAGGTGCAG 19

RESULT 9
 US-08-482-182-37
 ; Sequence 37, Application US/08482182
 ; Patent No. 5861273
 ; GENERAL INFORMATION:
 ; APPLICANT: MASCARENHAS, DESMOND

APPLICANT: OLSON, PAMELA S.
 TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,182
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.
 REGISTRATION NUMBER: 35,636
 REFERENCE/DOCKET NUMBER: 22095-20281.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 76 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-482-182-37

Query Match 1.0%; Score 15; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02; Mismatches 0; Gaps 0; Indels 0;

QY 1059 CATCTCTTTCCTT 1073
 Db 45 CATCTCTTTCCTT 59

RESULT 10
 US-08-482-182-36/c
 ; Sequence 36, Application US/08482182
 ; Patent No. 5861273
 ; GENERAL INFORMATION:
 ; APPLICANT: MASCARENHAS, DESMOND
 ; APPLICANT: OLSON, PAMELA S.
 ; TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,182
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PARK, FREDDIE K.

REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 22095-20281.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-482-182-36

Query Match 1.0%; Score 15; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1059 CATCTCTTTGCTT 1073
|||||
DB 40 CATCTCTTTGCTT 26

RESULT 11
US-08-411-796-283
; Sequence 283, Application US/08411796
; Patent No. 5677149
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mairé H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Polazzi, Joseph O.
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
; NUMBER OF SEQUENCES: 549
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/411,796
; FILING DATE: 22-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981044
; FILING DATE: 24-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11198
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C2713/1
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-471-039-283

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-411-796-283
Query Match 0.9%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1548 ATCTTGCTCTGCC 1561
|||||
DB 1 ATCTTGCTCTGCC 14
RESULT 12
US-08-471-039-283
; Sequence 283, Application US/08471039
; Patent No. 6017523
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mairé H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Polazzi, Joseph O.
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
; NUMBER OF SEQUENCES: 549
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/471,039
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981,044
; FILING DATE: 24-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11198
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C2713/5
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-471-039-283

Query Match 0.9%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1548 ATCTTGGTCTGTGCC 1561
| | | | | | | | | | | | | | | | | |
Db 1 ATCTTGGTCTGTGCC 14

RESULT 13
US-08-584-040-4455
; Sequence 4455, Application US/08584040
; Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4455:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4455

Query Match 0.9%; Score 14; DB 4; Length 18;
Best Local Similarity 78.6%; Pred. No. 3e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 945 GGGCCGCCCTCTGTG 958
| | | | | | | | | | | | | | | | | |
Db 3 GGGCCGCCUCUG 16

RESULT 14
PCT-US93-11198-283
; Sequence 283, Application PC/TUS9311198

GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Mairé H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Ollins, Peter O.
APPLICANT: Paik, Kumnan
APPLICANT: Polazzi, Joseph O.
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
NUMBER OF SEQUENCES: 549
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11198
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981044
FILING DATE: 24-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C2713/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 283:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
PCT-US93-11198-283

Query Match 0.9%; Score 14; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1548 ATCTTGGTCTGTGCC 1561
| | | | | | | | | | | | | | | | | |
Db 1 ATCTTGGTCTGTGCC 14

RESULT 15
US-09-851-520-54/C
; Sequence 54, Application US/09851520
; Patent No. 6399379
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
FILE REFERENCE: RTS-0241
CURRENT APPLICATION NUMBER: US/09/851,520
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 54
LENGTH: 20

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-520-54

Query Match      0.9%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 TTGATGAGCTGATG 345
Db 15 TTGATGAGCTGATG 2

Search completed: November 14, 2002, 20:55:54
Job time : 63 secs

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